

# SEQUENCE LISTING

<110> Friddle, Carl Johan  
Aylor, Erin  
Walke, D. Wade

<120> Novel Human Thrombospondin Repeat  
Proteins and Polynucleotides Encoding the Same

<130> LEX-0290-USA

<150> US 60/259,033

<151> 2000-12-28

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4398

<212> DNA

<213> homo sapiens

<400> 1

```

atggtgcgct gcattcagaa gctgaaccga actgtgggtg caaatgaaat atgcgaacac 60
tttgccttcc agcctcctac agaacagggt tgcctcattc cttgtccccc ggattgtgta 120
gtatctgagt tcttaccatg gtccaactgt agcaagggat gtgggaagaa attgcagcat 180
agaactcgcg cgggtcatagc tccccctctc tttggtggtt tgcaatgtcc aaatctgact 240
gagtcaagag cctgtgatgc tcccatttcc tgtcctcttg gggaagagga atatacattt 300
agccttaagg ttggaccatg gagtaaatgc agactgcctc atcttaaaga aattaatcca 360
agcgggaagaa ctgttctgga ttttaactct gattcaaatg agcgagtcac ctttaaacaat 420
caaagttaca aagcacatca tcattcgaag tcttgggcaa tagagatagg ttatcaaacc 480
cggcaggttt cgtgtacaag aagtgatgga caaaatgcta tgtaagcct ttgccttcaa 540
gattccttcc cattgactgt tcagtcctgc atcatgccca aagactgtga aacctccag 600
tggtcctcct ggagccccctg ctccaagaca tgcggttcag ggagtctctt gccaggattt 660
aggagcagga gccggaacgt gaagcacatg gctattggag gtggaaagga gtgtcctgaa 720
cttcttgaga aagaggcctg cattgttgaa ggagaacttc tgcagcaatg tcccaggat 780
tcttgagaaa cttctgaatg gaaagaatgc caagtctctc tctcctcga gcagcaggat 840
ccccactggc atgtgacggg acccgtgtgt ggcgggtggga tccagaccgg ggaggtgtac 900
tgtgcccgag gcgtaccagc agctgccgca ctgagggcca aggaagtctc tagacctgtg 960
gaaaaggcat tatgtgtggg acccgccccg ttgccctctc agctctgcaa tatcccttgc 1020
tctacggact gcatagtatc ttccctggta gcctggggcc tgtgcatcca tgaaaactgt 1080
catgaacctc aggggaaaaa aggatttaga acgaggcagc gccatgtcct catggaatct 1140
acagggcctg cagggcattg ccctcatttg gtggagtctg ttccctgtga ggatccaatg 1200
tgctaccgat ggctggcatc agaagggatc tgtttccctg atcatggaaa atgtggcctg 1260
ggacatcgta ttctgaaggc cgtctgccag aatgaccgag gagaagatgt atcaggagat 1320
ctttgccag ttccccctcc tctgagagg aagtcttctg aaattccctg ccgaatggac 1380
tgtgtgctga gcgagtggag ggagtggta tctgttccc agtcctgttc aaataaaaac 1440
tcagatggga aacagaccag gtcaagaact atcctggcac tggctgggga aggtggaaag 1500
ccatgtcccc ctagtcaggc tctccaagag catcgtttgt gtaatgacca ttctgttatg 1560
cagcttcaat gggagacatc gccttggggc ccttgttctg aggacacatt ggtaactgcc 1620
cttaatgcaa ccattggctg gaatggagaa gccacgtgtg gtgtaggcat tcagactcgg 1680
agagtcttct gtgtcaagag tcacgtggga caagtaatga ccaaaagatg tccagattct 1740
actcgacctg aaactgtgcg cccctgtttt ctcccatgca aaaaagactg tattgtgact 1800

```



		35					40				45								
Asn	Cys	Ser	Lys	Gly	Cys	Gly	Lys	Lys	Leu	Gln	His	Arg	Thr	Arg	Ala				
50						55					60								
Val	Ile	Ala	Pro	Pro	Leu	Phe	Gly	Gly	Leu	Gln	Cys	Pro	Asn	Leu	Thr				
65					70					75					80				
Glu	Ser	Arg	Ala	Cys	Asp	Ala	Pro	Ile	Ser	Cys	Pro	Leu	Gly	Glu	Glu				
				85					90					95					
Glu	Tyr	Thr	Phe	Ser	Leu	Lys	Val	Gly	Pro	Trp	Ser	Lys	Cys	Arg	Leu				
			100					105					110						
Pro	His	Leu	Lys	Glu	Ile	Asn	Pro	Ser	Gly	Arg	Thr	Val	Leu	Asp	Phe				
		115					120					125							
Asn	Ser	Asp	Ser	Asn	Glu	Arg	Val	Thr	Phe	Lys	His	Gln	Ser	Tyr	Lys				
130					135					140									
Ala	His	His	His	Ser	Lys	Ser	Trp	Ala	Ile	Glu	Ile	Gly	Tyr	Gln	Thr				
145					150					155					160				
Arg	Gln	Val	Ser	Cys	Thr	Arg	Ser	Asp	Gly	Gln	Asn	Ala	Met	Leu	Ser				
				165					170					175					
Leu	Cys	Leu	Gln	Asp	Ser	Phe	Pro	Leu	Thr	Val	Gln	Ser	Cys	Ile	Met				
			180					185					190						
Pro	Lys	Asp	Cys	Glu	Thr	Ser	Gln	Trp	Ser	Ser	Trp	Ser	Pro	Cys	Ser				
		195					200					205							
Lys	Thr	Cys	Arg	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Phe	Arg	Ser	Arg	Ser				
210					215					220									
Arg	Asn	Val	Lys	His	Met	Ala	Ile	Gly	Gly	Gly	Lys	Glu	Cys	Pro	Glu				
225					230					235					240				
Leu	Leu	Glu	Lys	Glu	Ala	Cys	Ile	Val	Glu	Gly	Glu	Leu	Leu	Gln	Gln				
				245					250					255					
Cys	Pro	Arg	Tyr	Ser	Trp	Arg	Thr	Ser	Glu	Trp	Lys	Glu	Cys	Gln	Val				
			260					265					270						
Ser	Leu	Leu	Leu	Glu	Gln	Gln	Asp	Pro	His	Trp	His	Val	Thr	Gly	Pro				
		275					280					285							
Val	Cys	Gly	Gly	Gly	Ile	Gln	Thr	Arg	Glu	Val	Tyr	Cys	Ala	Gln	Ser				
290						295					300								
Val	Pro	Ala	Ala	Ala	Ala	Leu	Arg	Ala	Lys	Glu	Val	Ser	Arg	Pro	Val				
305					310					315					320				
Glu	Lys	Ala	Leu	Cys	Val	Gly	Pro	Ala	Pro	Leu	Pro	Ser	Gln	Leu	Cys				
				325					330					335					
Asn	Ile	Pro	Cys	Ser	Thr	Asp	Cys	Ile	Val	Ser	Ser	Trp	Ser	Ala	Trp				
				340				345					350						
Gly	Leu	Cys	Ile	His	Glu	Asn	Cys	His	Glu	Pro	Gln	Gly	Lys	Lys	Gly				
		355					360					365							
Phe	Arg	Thr	Arg	Gln	Arg	His	Val	Leu	Met	Glu	Ser	Thr	Gly	Pro	Ala				
370						375						380							
Gly	His	Cys	Pro	His	Leu	Val	Glu	Ser	Val	Pro	Cys	Glu	Asp	Pro	Met				
385					390					395					400				
Cys	Tyr	Arg	Trp	Leu	Ala	Ser	Glu	Gly	Ile	Cys	Phe	Pro	Asp	His	Gly				
				405					410					415					
Lys	Cys	Gly	Leu	Gly	His	Arg	Ile	Leu	Lys	Ala	Val	Cys	Gln	Asn	Asp				
			420					425					430						
Arg	Gly	Glu	Asp	Val	Ser	Gly	Ser	Leu	Cys	Pro	Val	Pro	Pro	Pro	Pro				
		435					440					445							
Glu	Arg	Lys	Ser	Cys	Glu	Ile	Pro	Cys	Arg	Met	Asp	Cys	Val	Leu	Ser				
		450				455					460								
Glu	Trp	Thr	Glu	Trp	Ser	Ser	Cys	Ser	Gln	Ser	Cys	Ser	Asn	Lys	Asn				
465					470					475					480				
Ser	Asp	Gly	Lys	Gln	Thr	Arg	Ser	Arg	Thr	Ile	Leu	Ala	Leu	Ala	Gly				

				485					490				495				
Glu	Gly	Gly	Lys	Pro	Cys	Pro	Pro	Ser	Gln	Ala	Leu	Gln	Glu	His	Arg		
			500					505					510				
Leu	Cys	Asn	Asp	His	Ser	Cys	Met	Gln	Leu	His	Trp	Glu	Thr	Ser	Pro		
		515					520					525					
Trp	Gly	Pro	Cys	Ser	Glu	Asp	Thr	Leu	Val	Thr	Ala	Leu	Asn	Ala	Thr		
	530					535					540						
Ile	Gly	Trp	Asn	Gly	Glu	Ala	Thr	Cys	Gly	Val	Gly	Ile	Gln	Thr	Arg		
545				550					555						560		
Arg	Val	Phe	Cys	Val	Lys	Ser	His	Val	Gly	Gln	Val	Met	Thr	Lys	Arg		
			565					570						575			
Cys	Pro	Asp	Ser	Thr	Arg	Pro	Glu	Thr	Val	Arg	Pro	Cys	Phe	Leu	Pro		
		580					585					590					
Cys	Lys	Lys	Asp	Cys	Ile	Val	Thr	Ala	Phe	Ser	Glu	Trp	Thr	Pro	Cys		
		595				600					605						
Pro	Arg	Met	Cys	Gln	Ala	Gly	Asn	Ala	Thr	Val	Lys	Gln	Ser	Arg	Tyr		
	610					615				620							
Arg	Ile	Ile	Ile	Gln	Glu	Ala	Ala	Asn	Gly	Gly	Gln	Glu	Cys	Pro	Asp		
625				630					635						640		
Thr	Leu	Tyr	Glu	Glu	Arg	Glu	Cys	Glu	Asp	Val	Ser	Leu	Cys	Pro	Val		
			645					650						655			
Tyr	Arg	Trp	Lys	Pro	Gln	Lys	Trp	Ser	Pro	Cys	Ile	Leu	Val	Pro	Glu		
		660					665						670				
Ser	Val	Trp	Gln	Gly	Ile	Thr	Gly	Ser	Ser	Glu	Ala	Cys	Gly	Lys	Gly		
	675					680						685					
Leu	Gln	Thr	Arg	Ala	Val	Ser	Cys	Ile	Ser	Asp	Asp	Asn	Arg	Ser	Ala		
	690					695				700							
Glu	Met	Met	Glu	Cys	Leu	Lys	Gln	Thr	Asn	Gly	Met	Pro	Leu	Leu	Val		
705				710					715						720		
Gln	Glu	Cys	Thr	Val	Pro	Cys	Arg	Glu	Asp	Cys	Thr	Phe	Thr	Ala	Trp		
			725					730						735			
Ser	Lys	Phe	Thr	Pro	Cys	Ser	Thr	Asn	Cys	Glu	Ala	Thr	Lys	Ser	Arg		
		740					745						750				
Arg	Arg	Gln	Leu	Thr	Gly	Lys	Ser	Arg	Lys	Lys	Glu	Lys	Cys	Gln	Asp		
	755					760						765					
Ser	Asp	Leu	Tyr	Pro	Leu	Val	Glu	Thr	Glu	Leu	Cys	Pro	Cys	Asp	Glu		
	770					775					780						
Phe	Ile	Ser	Gln	Pro	Tyr	Gly	Asn	Trp	Ser	Asp	Cys	Ile	Leu	Pro	Glu		
785				790					795						800		
Gly	Arg	Arg	Glu	Pro	His	Arg	Gly	Leu	Arg	Val	Gln	Ala	Asp	Ser	Lys		
			805				810						815				
Glu	Cys	Gly	Glu	Gly	Leu	Arg	Phe	Arg	Ala	Val	Ala	Cys	Ser	Asp	Lys		
		820					825					830					
Asn	Gly	Arg	Pro	Val	Asp	Pro	Ser	Phe	Cys	Ser	Ser	Ser	Gly	Tyr	Ile		
	835					840						845					
Gln	Glu	Lys	Cys	Val	Ile	Pro	Cys	Pro	Phe	Asp	Cys	Lys	Leu	Ser	Asp		
	850					855					860						
Trp	Ser	Ser	Trp	Gly	Ser	Cys	Ser	Ser	Ser	Cys	Gly	Ile	Gly	Val	Arg		
865				870						875					880		
Ile	Arg	Ser	Lys	Trp	Leu	Lys	Glu	Lys	Pro	Tyr	Asn	Gly	Gly	Arg	Pro		
			885					890						895			
Cys	Pro	Lys	Leu	Asp	Leu	Lys	Asn	Gln	Val	His	Glu	Ala	Val	Pro	Cys		
		900					905						910				
Tyr	Ser	Glu	Cys	Asn	Gln	Tyr	Ser	Trp	Val	Val	Glu	His	Trp	Ser	Ser		
	915					920					925						
Cys	Lys	Ile	Asn	Asn	Glu	Leu	Arg	Ser	Leu	Arg	Cys	Gly	Gly	Gly	Thr		

930		935		940
Gln Ser Arg Lys Ile Arg Cys Val Asn Thr Ala Asp Gly Glu Gly Gly				
945		950		955
Ala Val Asp Ser Asn Leu Cys Asn Gln Asp Glu Ile Pro Pro Glu Thr				960
		965		970
				975
Gln Ser Cys Ser Leu Met Cys Pro Asn Glu Cys Val Met Ser Glu Trp				
		980		985
				990
Gly Leu Trp Ser Lys Cys Pro Gln Ser Cys Asp Pro His Thr Met Gln				
		995		1000
				1005
Arg Arg Thr Arg His Leu Leu Arg Pro Ser Leu Asn Ser Arg Thr Cys				
		1010		1015
				1020
Ala Glu Asp Ser Gln Val Gln Pro Cys Leu Leu Asn Glu Asn Cys Phe				
		1025		1030
				1035
Gln Phe Gln Tyr Asn Leu Thr Glu Trp Ser Thr Cys Gln Leu Ser Glu				
		1045		1050
				1055
Asn Ala Pro Cys Gly Gln Gly Val Arg Thr Arg Leu Leu Ser Cys Val				
		1060		1065
				1070
Cys Ser Asp Gly Lys Pro Val Ser Met Asp Gln Cys Glu Gln His Asn				
		1075		1080
				1085
Leu Glu Lys Pro Gln Arg Met Ser Ile Pro Cys Leu Val Glu Cys Val				
		1090		1095
				1100
Val Asn Cys Gln Leu Ser Gly Trp Thr Ala Trp Thr Glu Cys Ser Gln				
		1105		1110
				1115
Thr Cys Gly His Gly Gly Arg Met Ser Arg Thr Arg Phe Ile Ile Met				
		1125		1130
				1135
Pro Thr Gln Gly Glu Gly Arg Pro Cys Pro Thr Glu Leu Thr Gln Glu				
		1140		1145
				1150
Lys Thr Cys Pro Val Thr Pro Cys Tyr Ser Trp Val Leu Gly Asn Trp				
		1155		1160
				1165
Ser Ala Cys Lys Leu Glu Gly Gly Asp Cys Gly Glu Gly Val Gln Ile				
		1170		1175
				1180
Arg Ser Leu Ser Cys Met Val His Ser Gly Ser Ile Ser His Ala Ala				
		1185		1190
				1195
Gly Arg Val Glu Asp Ala Leu Cys Gly Glu Met Pro Phe Gln Asp Ser				
		1205		1210
				1215
Ile Leu Lys Gln Leu Cys Ser Val Pro Cys Pro Gly Asp Cys His Leu				
		1220		1225
				1230
Thr Glu Trp Ser Glu Trp Ser Thr Cys Glu Leu Thr Cys Ile Asp Gly				
		1235		1240
				1245
Arg Ser Phe Glu Thr Val Gly Arg Gln Ser Arg Ser Arg Thr Phe Ile				
		1250		1255
				1260
Ile Gln Ser Phe Glu Asn Gln Asp Ser Cys Pro Gln Gln Val Leu Glu				
		1265		1270
				1275
Thr Arg Pro Cys Thr Gly Gly Lys Cys Tyr His Tyr Thr Trp Lys Ala				
		1285		1290
				1295
Ser Leu Trp Asn Asn Asn Glu Arg Thr Val Trp Cys Gln Arg Ser Asp				
		1300		1305
				1310
Gly Val Asn Val Thr Gly Gly Cys Ser Pro Gln Ala Arg Pro Ala Ala				
		1315		1320
				1325
Ile Arg Gln Cys Ile Pro Ala Cys Arg Lys Pro Phe Ser Tyr Cys Thr				
		1330		1335
				1340
Gln Gly Gly Val Cys Gly Cys Glu Lys Gly Tyr Thr Glu Ile Met Lys				
		1345		1350
				1355
Ser Asn Gly Phe Leu Asp Tyr Cys Met Lys Val Pro Gly Ser Glu Asp				
		1365		1370
				1375
Lys Lys Ala Asp Val Lys Asn Leu Ser Gly Lys Asn Arg Pro Val Asn				

1380	1385	1390
Ser Lys Ile His Asp Ile Phe Lys Gly Trp Ser Leu Gln Pro Leu Asp		
1395	1400	1405
Pro Asp Gly Arg Val Lys Ile Trp Val Tyr Gly Val Ser Gly Gly Ala		
1410	1415	1420
Phe Leu Ile Met Ile Phe Leu Ile Phe Thr Ser Tyr Leu Val Cys Lys		
1425	1430	1435
Lys Pro Lys Pro His Gln Ser Thr Pro Pro Gln Gln Lys Pro Leu Thr		
1445	1450	1455
Leu Ala Tyr Asp Gly Asp Leu Asp Met		
1460	1465	

<210> 3  
 <211> 4773  
 <212> DNA  
 <213> homo sapiens

<400> 3

atgaggaagc	tctttctatt	gctttctctc	ttgctgtccc	atgcagctca	tttggaaggc	60
aaaaaggata	atcagttcat	ctggaaacca	ggctccgtgg	gaaggtgtac	aggagactgt	120
gggtcccgag	gagtcagag	tcgggcagtg	tggtgttttc	atgttgacgg	gtggacaagt	180
cacctgtcta	actgtgtga	gagcaacagg	cctccaaagg	aaagaagttg	tttccgagtt	240
tgtgactggc	acagtgcct	ctttcagtg	gaggtttctg	actggcacca	ctgtgtgctt	300
gttccttacg	ctcgcgtga	agtcaagcct	cggactgcag	agtgtgtgac	ggctcagcat	360
ggactgcagc	accgatggg	gcgctgcatt	cagaagctga	accgaactgt	ggttgcaaat	420
gaaatatgcg	aacactttgc	ccttcagcct	cctacagaac	aggcttgctt	cattccttgt	480
ccccgggatt	gtgtagtatc	tgagttctta	ccatgggtcca	actgtagcaa	gggatgtggg	540
aagaaattgc	agcatagaac	tcgcgcgggc	atagctcccc	ctctcttttg	tggtttgcaa	600
tgtccaaatc	tgactgagtc	aagagcctgt	gatgctccca	tttctgtgcc	tcttggggaa	660
gaggaatata	catttagcct	taagggttga	ccatggagta	aatgcagact	gcctcatctt	720
aaagaaatta	atccaagcgg	aagaactggt	ctggatttta	actctgattc	aaatgagcga	780
gtcaccttta	aacatcaaag	ttacaaagca	catcatcatt	cgaagtcttg	ggcaatagag	840
ataggttatc	aaaccgggca	ggtttcgtgt	acaagaagtg	atggacaaaa	tgctatgtta	900
agcctttgcc	ttcaagattc	cttcccattg	actgttcagt	cctgcatcat	gccccaaagc	960
tgtgaaacct	cccagtgggc	ctcctggagc	ccctgctcca	agacatgccg	ttcagggagt	1020
ctcttgccag	gatttaggag	caggagccgg	aacgtgaagc	acatggctat	tggaggtgga	1080
aaggagtgtc	ctgaacttct	tgagaaagag	gcctgcattg	ttgaaggaga	acttctgcag	1140
caatgtccca	ggtattcctg	gagaacttct	gaatggaaag	aatgccaagt	ctctctcttc	1200
ctcgagcagc	aggatcccca	ctggcatgtg	acgggacccg	tgtgtggcgg	tgggatccag	1260
acccgggagg	tgtactgtgc	ccagagcgta	ccagcagctg	ccgcactgag	ggccaaggaa	1320
gtctctagac	ctgtggaaaa	ggcattatgt	gtgggacccg	ccccgttgcc	ctctcagctc	1380
tgcaatatcc	cttgctctac	ggactgcata	gtatcttctt	ggtcagcctg	gggcctgtgc	1440
atccatgaaa	actgtcatga	acctcagggg	aaaaaaggat	ttagaacgag	gcagcgccat	1500
gtcctcatgg	aatctacagg	gcctgcaggg	cattgccctc	atttggtgga	gtctgttctt	1560
tgtgaggatc	caatgtgcta	ccgatggctg	gcatacagaag	ggatctgttt	ccctgatcat	1620
ggaaaatgtg	gcctgggaca	tcgtattctg	aaggccgtct	gccagaatga	ccgcggagaa	1680
gatgtatcag	ggagtctttg	cccagttccc	cctcctcctg	agaggaagtc	ttgtgaaatt	1740
ccctgccgaa	tggactgtgt	gctgagcgag	tggacggagt	ggcatcctg	ttcccagctc	1800
tggtcaataa	aaaactcaga	accaggtcaa	gaactatcct	ggcactggct		1860
ggggaaggtg	gaaagccatg	tccccctagt	caggctctcc	aagagcatcg	tttgtgtaat	1920
gaccattcct	gtatgcagct	tactggggag	acatcgccct	ggggcccttg	ttctgaggac	1980
acattggtaa	ctgcccttaa	tgcaaccatt	ggctggaatg	gagaagccac	gtgtggtgta	2040
ggcattcaga	ctcggagagt	cttctgtgtc	aagagtcacg	tgggacaagt	aatgacaaa	2100
agatgtccag	attctactcg	acctgaaact	gtgcgcccct	gttttctccc	atgcaaaaaa	2160
gactgtattg	tgactgcttt	cagtgagtgg	acaccctgcc	caaggatgtg	ccaagcagga	2220

```

aatgccacag taaaacagtc tcgatacaga atcatcatcc aagaagcagc caatggaggc 2280
caggaatgcc cagatacctt atatgaggag agagagtgtg aagatgtttc cttgtgtcct 2340
gtatatcggt ggaagccaca gaaatggagc cttgcatct tagtgccaga gtctgtctgg 2400
caggggaataa cgggcagcag tgaagcctgt ggaaggggt tacaacaag agctgtctca 2460
tgcattctctg atgacaaccg gtcagcagaa atgatggaat gcctcaagca gacaaacggc 2520
atgcctctcc ttgtgcaaga atgcacagtc ccatgtcgag aagactgcac cttcactgct 2580
tggtccaagt ttacgccctg ctccacgaac tgtgaagcca caaaaagtag gcggcgacag 2640
ctcacaggga aaagcagaaa gaaggagaaa tgccaggatt ctgaccttta ccctctagt 2700
gagacagaac tatgtccttg tgatgaattt atatcccaac cttatggaaa ctggtcagat 2760
tgcattcttc cagaaggcag aagggagcct caccgaggac tgcgggtaca agcagacagc 2820
aaagaatgtg gagaaggcct gcgctttcga gcagtagcct gttctgataa aaatggaaga 2880
cctgttgacc cctccttctg cagcagctct ggttacattc aagaaaaatg tgtcattccc 2940
tgcccatttg attgcaagtt aagcgattgg tctagtggg ggtcttgca ttcattctgt 3000
ggaattggag tgagaattcg atccaaatgg ctaaaagaaa aaccttaca tggaggacga 3060
ccatgtccca aactggatct caagaatcag gtacatgagg cagtcccatg ttacagtga 3120
tgcaatcagt attcctgggt tgtagaacac tggcttcat gcaaaatcaa caatgagctg 3180
aggtcctgc gctgtggagg aggaacacaa tctaggaaaa tcagatgtgt gaatactgcg 3240
gatggtgaag gtggagcagt ggatagcaac ctgtgcaacc aggatgaaat tccccagaa 3300
accagtcct gttctcttat gtgtcccaat gagtgtgtca tgtctgagt gggactttgg 3360
agcaaatgcc cacagtcatg cgatccccac acaatgcaga gaagaactcg ccacctgcta 3420
agaccatcac tgaactcaag gacttgtgct gaagactcac aggtgcagcc ttgcctcctg 3480
aatgaaaatt gcttcagtt ccagtacaat ctaacagagt ggagcacatg ccagctgagt 3540
gaaaacgcac cctgtggtca aggcgtcagg accgcctgc taagctgtgt gtgcagtgat 3600
ggcaagccag tcagcatgga ccaatgtgag cagcataatt tggagaagcc ccagagaatg 3660
agcattccct gcttgggtga atgcgtggtc aactgtcagc tctcaggggtg gacggcttgg 3720
acagagtgtt cacagacctg tggccatgga ggtcgaatga gccggactcg atttatcatt 3780
atgccaaacc aaggagaagg acggccatgc cccacagagc ttaccagga gaaaacctgc 3840
ccagtgaacc cctgctacag ctgggtcctt ggcaactggt ctgcatgtaa attggagggt 3900
ggagactgtg ggaaggagt tcagatccgc agcctttcct gcatggtcca cagtggttca 3960
atatctcatg cagctggacg tgtcgaggat gactgtgtg gagaaatgcc ctttcaggac 4020
agcatcctga agcagctgtg ttctgtgcct tgcccaggag actgccattt aacagaatgg 4080
tcagagtgga gcacatgtga attaacctgc attgatggaa gaagctttga gactgtgggc 4140
cgcaggtcta gatcaaggac ttttataatt cagtcttttg agaaccaaga cagctgcccc 4200
caacaggttc tagaaacacg cccttgtaca ggaggcaaat gttatcacta cacatggaaa 4260
gcaagtcttt ggaacaataa cgaacgaact gtatggtgcc agcgttcaga tggcgtaaat 4320
gtcacaggag gctgtcccc tcaggcccgt cctgctgcca ttcggcagtg cattccagcc 4380
tgcagaaaac ctttctccta ctgtacacag ggtggagtct gtggttgtga gaagggctat 4440
acagagataa tgaatcaaaa tggtttctct gattactgca tgaaagtacc aggtcagag 4500
gataaaaaag ctgatgtgaa aaacctttct gggaaaaaca gacctgtgaa ttcaaaaata 4560
catgatattt ttaaaggatg gtctcttcaa ccacttgatc cagatggccg agtaaaaatt 4620
tgggtttatg gcgtttcagg tggcgctttt ctcatcatga ttttctaata atttacttcc 4680
taccttgttt gcaagaagcc aaaaccacat caaagcacac ctccccaaca gaagcctctg 4740
accttagcct acgatggaga cttagacatg taa 4773

```

```

<210> 4
<211> 1590
<212> PRT
<213> homo sapiens

```

```

<400> 4
Met Arg Lys Leu Phe Leu Leu Leu Ser Leu Leu Leu Ser His Ala Ala
  1             5             10             15
His Leu Glu Gly Lys Lys Asp Asn Gln Phe Ile Trp Lys Pro Gly Pro
      20             25             30
Trp Gly Arg Cys Thr Gly Asp Cys Gly Pro Gly Gly Val Gln Ser Arg
      35             40             45

```

Ala	Val	Trp	Cys	Phe	His	Val	Asp	Gly	Trp	Thr	Ser	His	Leu	Ser	Asn	50	55	60
Cys	Gly	Glu	Ser	Asn	Arg	Pro	Pro	Lys	Glu	Arg	Ser	Cys	Phe	Arg	Val	65	70	75
Cys	Asp	Trp	His	Ser	Asp	Leu	Phe	Gln	Trp	Glu	Val	Ser	Asp	Trp	His	85	90	95
His	Cys	Val	Leu	Val	Pro	Tyr	Ala	Arg	Gly	Glu	Val	Lys	Pro	Arg	Thr	100	105	110
Ala	Glu	Cys	Val	Thr	Ala	Gln	His	Gly	Leu	Gln	His	Arg	Met	Val	Arg	115	120	125
Cys	Ile	Gln	Lys	Leu	Asn	Arg	Thr	Val	Val	Ala	Asn	Glu	Ile	Cys	Glu	130	135	140
His	Phe	Ala	Leu	Gln	Pro	Pro	Thr	Glu	Gln	Ala	Cys	Leu	Ile	Pro	Cys	145	150	155
Pro	Arg	Asp	Cys	Val	Val	Ser	Glu	Phe	Leu	Pro	Trp	Ser	Asn	Cys	Ser	165	170	175
Lys	Gly	Cys	Gly	Lys	Lys	Leu	Gln	His	Arg	Thr	Arg	Ala	Val	Ile	Ala	180	185	190
Pro	Pro	Leu	Phe	Gly	Gly	Leu	Gln	Cys	Pro	Asn	Leu	Thr	Glu	Ser	Arg	195	200	205
Ala	Cys	Asp	Ala	Pro	Ile	Ser	Cys	Pro	Leu	Gly	Glu	Glu	Glu	Tyr	Thr	210	215	220
Phe	Ser	Leu	Lys	Val	Gly	Pro	Trp	Ser	Lys	Cys	Arg	Leu	Pro	His	Leu	225	230	235
Lys	Glu	Ile	Asn	Pro	Ser	Gly	Arg	Thr	Val	Leu	Asp	Phe	Asn	Ser	Asp	245	250	255
Ser	Asn	Glu	Arg	Val	Thr	Phe	Lys	His	Gln	Ser	Tyr	Lys	Ala	His	His	260	265	270
His	Ser	Lys	Ser	Trp	Ala	Ile	Glu	Ile	Gly	Tyr	Gln	Thr	Arg	Gln	Val	275	280	285
Ser	Cys	Thr	Arg	Ser	Asp	Gly	Gln	Asn	Ala	Met	Leu	Ser	Leu	Cys	Leu	290	295	300
Gln	Asp	Ser	Phe	Pro	Leu	Thr	Val	Gln	Ser	Cys	Ile	Met	Pro	Lys	Asp	305	310	315
Cys	Glu	Thr	Ser	Gln	Trp	Ser	Ser	Trp	Ser	Pro	Cys	Ser	Lys	Thr	Cys	325	330	335
Arg	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Phe	Arg	Ser	Arg	Ser	Arg	Asn	Val	340	345	350
Lys	His	Met	Ala	Ile	Gly	Gly	Gly	Lys	Glu	Cys	Pro	Glu	Leu	Leu	Glu	355	360	365
Lys	Glu	Ala	Cys	Ile	Val	Glu	Gly	Glu	Leu	Leu	Gln	Gln	Cys	Pro	Arg	370	375	380
Tyr	Ser	Trp	Arg	Thr	Ser	Glu	Trp	Lys	Glu	Cys	Gln	Val	Ser	Leu	Leu	385	390	395
Leu	Glu	Gln	Gln	Asp	Pro	His	Trp	His	Val	Thr	Gly	Pro	Val	Cys	Gly	405	410	415
Gly	Gly	Ile	Gln	Thr	Arg	Glu	Val	Tyr	Cys	Ala	Gln	Ser	Val	Pro	Ala	420	425	430
Ala	Ala	Ala	Leu	Arg	Ala	Lys	Glu	Val	Ser	Arg	Pro	Val	Glu	Lys	Ala	435	440	445
Leu	Cys	Val	Gly	Pro	Ala	Pro	Leu	Pro	Ser	Gln	Leu	Cys	Asn	Ile	Pro	450	455	460
Cys	Ser	Thr	Asp	Cys	Ile	Val	Ser	Ser	Trp	Ser	Ala	Trp	Gly	Leu	Cys	465	470	475
Ile	His	Glu	Asn	Cys	His	Glu	Pro	Gln	Gly	Lys	Lys	Gly	Phe	Arg	Thr	485	490	495



Arg	Gln	Arg	His	Val	Leu	Met	Glu	Ser	Thr	Gly	Pro	Ala	Gly	His	Cys	
			500					505					510			
Pro	His	Leu	Val	Glu	Ser	Val	Pro	Cys	Glu	Asp	Pro	Met	Cys	Tyr	Arg	
		515					520					525				
Trp	Leu	Ala	Ser	Glu	Gly	Ile	Cys	Phe	Pro	Asp	His	Gly	Lys	Cys	Gly	
	530					535					540					
Leu	Gly	His	Arg	Ile	Leu	Lys	Ala	Val	Cys	Gln	Asn	Asp	Arg	Gly	Glu	
545					550					555					560	
Asp	Val	Ser	Gly	Ser	Leu	Cys	Pro	Val	Pro	Pro	Pro	Pro	Glu	Arg	Lys	
			565						570					575		
Ser	Cys	Glu	Ile	Pro	Cys	Arg	Met	Asp	Cys	Val	Leu	Ser	Glu	Trp	Thr	
			580					585						590		
Glu	Trp	Ser	Ser	Cys	Ser	Gln	Ser	Cys	Ser	Asn	Lys	Asn	Ser	Asp	Gly	
	595					600						605				
Lys	Gln	Thr	Arg	Ser	Arg	Thr	Ile	Leu	Ala	Leu	Ala	Gly	Glu	Gly	Gly	
	610					615					620					
Lys	Pro	Cys	Pro	Pro	Ser	Gln	Ala	Leu	Gln	Glu	His	Arg	Leu	Cys	Asn	
625					630					635					640	
Asp	His	Ser	Cys	Met	Gln	Leu	His	Trp	Glu	Thr	Ser	Pro	Trp	Gly	Pro	
			645						650					655		
Cys	Ser	Glu	Asp	Thr	Leu	Val	Thr	Ala	Leu	Asn	Ala	Thr	Ile	Gly	Trp	
			660					665					670			
Asn	Gly	Glu	Ala	Thr	Cys	Gly	Val	Gly	Ile	Gln	Thr	Arg	Arg	Val	Phe	
	675					680						685				
Cys	Val	Lys	Ser	His	Val	Gly	Gln	Val	Met	Thr	Lys	Arg	Cys	Pro	Asp	
	690					695					700					
Ser	Thr	Arg	Pro	Glu	Thr	Val	Arg	Pro	Cys	Phe	Leu	Pro	Cys	Lys	Lys	
705					710					715					720	
Asp	Cys	Ile	Val	Thr	Ala	Phe	Ser	Glu	Trp	Thr	Pro	Cys	Pro	Arg	Met	
			725						730					735		
Cys	Gln	Ala	Gly	Asn	Ala	Thr	Val	Lys	Gln	Ser	Arg	Tyr	Arg	Ile	Ile	
		740						745					750			
Ile	Gln	Glu	Ala	Ala	Asn	Gly	Gly	Gln	Glu	Cys	Pro	Asp	Thr	Leu	Tyr	
	755					760						765				
Glu	Glu	Arg	Glu	Cys	Glu	Asp	Val	Ser	Leu	Cys	Pro	Val	Tyr	Arg	Trp	
	770					775					780					
Lys	Pro	Gln	Lys	Trp	Ser	Pro	Cys	Ile	Leu	Val	Pro	Glu	Ser	Val	Trp	
785					790					795					800	
Gln	Gly	Ile	Thr	Gly	Ser	Ser	Glu	Ala	Cys	Gly	Lys	Gly	Leu	Gln	Thr	
			805						810					815		
Arg	Ala	Val	Ser	Cys	Ile	Ser	Asp	Asp	Asn	Arg	Ser	Ala	Glu	Met	Met	
			820					825					830			
Glu	Cys	Leu	Lys	Gln	Thr	Asn	Gly	Met	Pro	Leu	Leu	Val	Gln	Glu	Cys	
	835						840						845			
Thr	Val	Pro	Cys	Arg	Glu	Asp	Cys	Thr	Phe	Thr	Ala	Trp	Ser	Lys	Phe	
	850					855					860					
Thr	Pro	Cys	Ser	Thr	Asn	Cys	Glu	Ala	Thr	Lys	Ser	Arg	Arg	Arg	Gln	
865					870					875					880	
Leu	Thr	Gly	Lys	Ser	Arg	Lys	Lys	Glu	Lys	Cys	Gln	Asp	Ser	Asp	Leu	
			885						890					895		
Tyr	Pro	Leu	Val	Glu	Thr	Glu	Leu	Cys	Pro	Cys	Asp	Glu	Phe	Ile	Ser	
		900						905					910			
Gln	Pro	Tyr	Gly	Asn	Trp	Ser	Asp	Cys	Ile	Leu	Pro	Glu	Gly	Arg	Arg	
	915						920					925				
Glu	Pro	His	Arg	Gly	Leu	Arg	Val	Gln	Ala	Asp	Ser	Lys	Glu	Cys	Gly	
	930					935						940				

Glu	Gly	Leu	Arg	Phe	Arg	Ala	Val	Ala	Cys	Ser	Asp	Lys	Asn	Gly	Arg	945	950	955	960
Pro	Val	Asp	Pro	Ser	Phe	Cys	Ser	Ser	Ser	Gly	Tyr	Ile	Gln	Glu	Lys		965	970	975
Cys	Val	Ile	Pro	Cys	Pro	Phe	Asp	Cys	Lys	Leu	Ser	Asp	Trp	Ser	Ser		980	985	990
Trp	Gly	Ser	Cys	Ser	Ser	Ser	Cys	Gly	Ile	Gly	Val	Arg	Ile	Arg	Ser		995	1000	1005
Lys	Trp	Leu	Lys	Glu	Lys	Pro	Tyr	Asn	Gly	Gly	Arg	Pro	Cys	Pro	Lys		1010	1015	1020
Leu	Asp	Leu	Lys	Asn	Gln	Val	His	Glu	Ala	Val	Pro	Cys	Tyr	Ser	Glu		1025	1030	1035
Cys	Asn	Gln	Tyr	Ser	Trp	Val	Val	Glu	His	Trp	Ser	Ser	Cys	Lys	Ile		1045	1050	1055
Asn	Asn	Glu	Leu	Arg	Ser	Leu	Arg	Cys	Gly	Gly	Gly	Thr	Gln	Ser	Arg		1060	1065	1070
Lys	Ile	Arg	Cys	Val	Asn	Thr	Ala	Asp	Gly	Glu	Gly	Gly	Ala	Val	Asp		1075	1080	1085
Ser	Asn	Leu	Cys	Asn	Gln	Asp	Glu	Ile	Pro	Pro	Glu	Thr	Gln	Ser	Cys		1090	1095	1100
Ser	Leu	Met	Cys	Pro	Asn	Glu	Cys	Val	Met	Ser	Glu	Trp	Gly	Leu	Trp		1105	1110	1115
Ser	Lys	Cys	Pro	Gln	Ser	Cys	Asp	Pro	His	Thr	Met	Gln	Arg	Arg	Thr		1125	1130	1135
Arg	His	Leu	Leu	Arg	Pro	Ser	Leu	Asn	Ser	Arg	Thr	Cys	Ala	Glu	Asp		1140	1145	1150
Ser	Gln	Val	Gln	Pro	Cys	Leu	Leu	Asn	Glu	Asn	Cys	Phe	Gln	Phe	Gln		1155	1160	1165
Tyr	Asn	Leu	Thr	Glu	Trp	Ser	Thr	Cys	Gln	Leu	Ser	Glu	Asn	Ala	Pro		1170	1175	1180
Cys	Gly	Gln	Gly	Val	Arg	Thr	Arg	Leu	Leu	Ser	Cys	Val	Cys	Ser	Asp		1185	1190	1195
Gly	Lys	Pro	Val	Ser	Met	Asp	Gln	Cys	Glu	Gln	His	Asn	Leu	Glu	Lys		1205	1210	1215
Pro	Gln	Arg	Met	Ser	Ile	Pro	Cys	Leu	Val	Glu	Cys	Val	Val	Asn	Cys		1220	1225	1230
Gln	Leu	Ser	Gly	Trp	Thr	Ala	Trp	Thr	Glu	Cys	Ser	Gln	Thr	Cys	Gly		1235	1240	1245
His	Gly	Gly	Arg	Met	Ser	Arg	Thr	Arg	Phe	Ile	Ile	Met	Pro	Thr	Gln		1250	1255	1260
Gly	Glu	Gly	Arg	Pro	Cys	Pro	Thr	Glu	Leu	Thr	Gln	Glu	Lys	Thr	Cys		1265	1270	1275
Pro	Val	Thr	Pro	Cys	Tyr	Ser	Trp	Val	Leu	Gly	Asn	Trp	Ser	Ala	Cys		1285	1290	1295
Lys	Leu	Glu	Gly	Gly	Asp	Cys	Gly	Glu	Gly	Val	Gln	Ile	Arg	Ser	Leu		1300	1305	1310
Ser	Cys	Met	Val	His	Ser	Gly	Ser	Ile	Ser	His	Ala	Ala	Gly	Arg	Val		1315	1320	1325
Glu	Asp	Ala	Leu	Cys	Gly	Glu	Met	Pro	Phe	Gln	Asp	Ser	Ile	Leu	Lys		1330	1335	1340
Gln	Leu	Cys	Ser	Val	Pro	Cys	Pro	Gly	Asp	Cys	His	Leu	Thr	Glu	Trp		1345	1350	1355
Ser	Glu	Trp	Ser	Thr	Cys	Glu	Leu	Thr	Cys	Ile	Asp	Gly	Arg	Ser	Phe		1365	1370	1375
Glu	Thr	Val	Gly	Arg	Gln	Ser	Arg	Ser	Arg	Thr	Phe	Ile	Ile	Gln	Ser		1380	1385	1390

Phe Glu Asn Gln Asp Ser Cys Pro Gln Gln Val Leu Glu Thr Arg Pro  
 1395 1400 1405  
 Cys Thr Gly Gly Lys Cys Tyr His Tyr Thr Trp Lys Ala Ser Leu Trp  
 1410 1415 1420  
 Asn Asn Asn Glu Arg Thr Val Trp Cys Gln Arg Ser Asp Gly Val Asn  
 1425 1430 1435 1440  
 Val Thr Gly Gly Cys Ser Pro Gln Ala Arg Pro Ala Ala Ile Arg Gln  
 1445 1450 1455  
 Cys Ile Pro Ala Cys Arg Lys Pro Phe Ser Tyr Cys Thr Gln Gly Gly  
 1460 1465 1470  
 Val Cys Gly Cys Glu Lys Gly Tyr Thr Glu Ile Met Lys Ser Asn Gly  
 1475 1480 1485  
 Phe Leu Asp Tyr Cys Met Lys Val Pro Gly Ser Glu Asp Lys Lys Ala  
 1490 1495 1500  
 Asp Val Lys Asn Leu Ser Gly Lys Asn Arg Pro Val Asn Ser Lys Ile  
 1505 1510 1515 1520  
 His Asp Ile Phe Lys Gly Trp Ser Leu Gln Pro Leu Asp Pro Asp Gly  
 1525 1530 1535  
 Arg Val Lys Ile Trp Val Tyr Gly Val Ser Gly Gly Ala Phe Leu Ile  
 1540 1545 1550  
 Met Ile Phe Leu Ile Phe Thr Ser Tyr Leu Val Cys Lys Lys Pro Lys  
 1555 1560 1565  
 Pro His Gln Ser Thr Pro Pro Gln Gln Lys Pro Leu Thr Leu Ala Tyr  
 1570 1575 1580  
 Asp Gly Asp Leu Asp Met  
 1585 1590

<210> 5  
 <211> 4821  
 <212> DNA  
 <213> homo sapiens

<400> 5  
 atgtttccaa agagcaacct aacagtcact tgctgggtat ggaggagcat gaggaagctc 60  
 tttctattgc tttctctctt gctgtcccat gcagctcatt tggaaggcaa aaaggataat 120  
 cagttcatct ggaaaccagg tccgtgggga aggtgtacag gagactgtgg tcccggagga 180  
 gtccagagtc gggcagtggt gtgttttcat gttgacgggt ggacaagtca cctgtctaac 240  
 tgtggtgaga gcaacaggcc tcaaaggaa agaagttgtt tccgagtttg tgactggcac 300  
 agtgacctct ttcagtgga ggtttctgac tggcaccact gtgtgcttgt tccttacgct 360  
 cgcggtgaag tcaagcctcg gactgcagag tgtgtgacgg ctcagcatgg actgcagcac 420  
 cggatggtgc gctgcattca gaagctgaac cgaactgtgg ttgcaaatga aatatgcgaa 480  
 cactttgccc ttcagcctcc tacagaacag gcttgccctca ttccttgtcc ccgggattgt 540  
 gtagtatctg agttcttacc atggtccaac tgtagcaagg gatgtgggaa gaaattgcag 600  
 catagaactc gcgcggtcat agctccccct ctctttggtg gtttgcaatg tccaaatctg 660  
 actgagtcaa gagectgtga tgctcccat tctgtctctc ttggggaaga ggaatataca 720  
 tttagcctta aggttgacc atggagtaaa tgcagactgc ctcactctaa agaaattaat 780  
 ccaagcggaa gaactgttct ggattttaac tctgattcaa atgagcgagt cacctttaaa 840  
 catcaaagtt acaaagcaca tcatcattcg aagtcttggg caatagagat aggttatcaa 900  
 acccggcagg tttcgtgtac aagaagtgat ggacaaaatg ctatgttaag cctttgcctt 960  
 caagattcct tcccattgac tgttcagtcc tgcacatgc ccaaagactg tgaaacctcc 1020  
 cagtggctcct cctggagccc ctgctccaag acatgccgtt caggaggtct cttgccagga 1080  
 tttaggagca ggagccggaa cgtgaagcac atggctattg gaggtggaaa ggagtgtcct 1140  
 gaacttcttg agaaagaggc ctgcattgtt gaaggagaac ttctgcagca atgtcccagg 1200  
 tattcctgga gaacttctga atggaaagaa tgccaagtct ctctctcct cgagcagcag 1260  
 gatccccact ggcattgtgac gggaccctgt tgtggcggtg ggatccagac ccgggaggtg 1320



gtttcagggtg ggcgttttct catcatgatt ttctaatat ttacttccta ccttggttgc 4740  
aagaagccaa aaccacatca aagcacacct ccccaacaga agcctctgac cttagcctac 4800  
gatggagact tagacatgta a 4821

<210> 6  
<211> 1606  
<212> PRT  
<213> homo sapiens

<400> 6  
Met Phe Pro Lys Ser Asn Leu Thr Val Thr Cys Trp Val Trp Arg Ser  
1 5 10 15  
Met Arg Lys Leu Phe Leu Leu Leu Ser Leu Leu Leu Ser His Ala Ala  
20 25 30  
His Leu Glu Gly Lys Lys Asp Asn Gln Phe Ile Trp Lys Pro Gly Pro  
35 40 45  
Trp Gly Arg Cys Thr Gly Asp Cys Gly Pro Gly Gly Val Gln Ser Arg  
50 55 60  
Ala Val Trp Cys Phe His Val Asp Gly Trp Thr Ser His Leu Ser Asn  
65 70 75 80  
Cys Gly Glu Ser Asn Arg Pro Pro Lys Glu Arg Ser Cys Phe Arg Val  
85 90 95  
Cys Asp Trp His Ser Asp Leu Phe Gln Trp Glu Val Ser Asp Trp His  
100 105 110  
His Cys Val Leu Val Pro Tyr Ala Arg Gly Glu Val Lys Pro Arg Thr  
115 120 125  
Ala Glu Cys Val Thr Ala Gln His Gly Leu Gln His Arg Met Val Arg  
130 135 140  
Cys Ile Gln Lys Leu Asn Arg Thr Val Val Ala Asn Glu Ile Cys Glu  
145 150 155 160  
His Phe Ala Leu Gln Pro Pro Thr Glu Gln Ala Cys Leu Ile Pro Cys  
165 170 175  
Pro Arg Asp Cys Val Val Ser Glu Phe Leu Pro Trp Ser Asn Cys Ser  
180 185 190  
Lys Gly Cys Gly Lys Lys Leu Gln His Arg Thr Arg Ala Val Ile Ala  
195 200 205  
Pro Pro Leu Phe Gly Gly Leu Gln Cys Pro Asn Leu Thr Glu Ser Arg  
210 215 220  
Ala Cys Asp Ala Pro Ile Ser Cys Pro Leu Gly Glu Glu Glu Tyr Thr  
225 230 235 240  
Phe Ser Leu Lys Val Gly Pro Trp Ser Lys Cys Arg Leu Pro His Leu  
245 250 255  
Lys Glu Ile Asn Pro Ser Gly Arg Thr Val Leu Asp Phe Asn Ser Asp  
260 265 270  
Ser Asn Glu Arg Val Thr Phe Lys His Gln Ser Tyr Lys Ala His His  
275 280 285  
His Ser Lys Ser Trp Ala Ile Glu Ile Gly Tyr Gln Thr Arg Gln Val  
290 295 300  
Ser Cys Thr Arg Ser Asp Gly Gln Asn Ala Met Leu Ser Leu Cys Leu  
305 310 315 320  
Gln Asp Ser Phe Pro Leu Thr Val Gln Ser Cys Ile Met Pro Lys Asp  
325 330 335  
Cys Glu Thr Ser Gln Trp Ser Ser Trp Ser Pro Cys Ser Lys Thr Cys  
340 345 350  
Arg Ser Gly Ser Leu Leu Pro Gly Phe Arg Ser Arg Ser Arg Asn Val  
355 360 365

Lys His Met Ala Ile Gly Gly Gly Lys Glu Cys Pro Glu Leu Leu Glu  
 370 375 380  
 Lys Glu Ala Cys Ile Val Glu Gly Glu Leu Leu Gln Gln Cys Pro Arg  
 385 390 395 400  
 Tyr Ser Trp Arg Thr Ser Glu Trp Lys Glu Cys Gln Val Ser Leu Leu  
 405 410 415  
 Leu Glu Gln Gln Asp Pro His Trp His Val Thr Gly Pro Val Cys Gly  
 420 425 430  
 Gly Gly Ile Gln Thr Arg Glu Val Tyr Cys Ala Gln Ser Val Pro Ala  
 435 440 445  
 Ala Ala Ala Leu Arg Ala Lys Glu Val Ser Arg Pro Val Glu Lys Ala  
 450 455 460  
 Leu Cys Val Gly Pro Ala Pro Leu Pro Ser Gln Leu Cys Asn Ile Pro  
 465 470 475 480  
 Cys Ser Thr Asp Cys Ile Val Ser Ser Trp Ser Ala Trp Gly Leu Cys  
 485 490 495  
 Ile His Glu Asn Cys His Glu Pro Gln Gly Lys Lys Gly Phe Arg Thr  
 500 505 510  
 Arg Gln Arg His Val Leu Met Glu Ser Thr Gly Pro Ala Gly His Cys  
 515 520 525  
 Pro His Leu Val Glu Ser Val Pro Cys Glu Asp Pro Met Cys Tyr Arg  
 530 535 540  
 Trp Leu Ala Ser Glu Gly Ile Cys Phe Pro Asp His Gly Lys Cys Gly  
 545 550 555 560  
 Leu Gly His Arg Ile Leu Lys Ala Val Cys Gln Asn Asp Arg Gly Glu  
 565 570 575  
 Asp Val Ser Gly Ser Leu Cys Pro Val Pro Pro Pro Pro Glu Arg Lys  
 580 585 590  
 Ser Cys Glu Ile Pro Cys Arg Met Asp Cys Val Leu Ser Glu Trp Thr  
 595 600 605  
 Glu Trp Ser Ser Cys Ser Gln Ser Cys Ser Asn Lys Asn Ser Asp Gly  
 610 615 620  
 Lys Gln Thr Arg Ser Arg Thr Ile Leu Ala Leu Ala Gly Glu Gly Gly  
 625 630 635 640  
 Lys Pro Cys Pro Pro Ser Gln Ala Leu Gln Glu His Arg Leu Cys Asn  
 645 650 655  
 Asp His Ser Cys Met Gln Leu His Trp Glu Thr Ser Pro Trp Gly Pro  
 660 665 670  
 Cys Ser Glu Asp Thr Leu Val Thr Ala Leu Asn Ala Thr Ile Gly Trp  
 675 680 685  
 Asn Gly Glu Ala Thr Cys Gly Val Gly Ile Gln Thr Arg Arg Val Phe  
 690 695 700  
 Cys Val Lys Ser His Val Gly Gln Val Met Thr Lys Arg Cys Pro Asp  
 705 710 715 720  
 Ser Thr Arg Pro Glu Thr Val Arg Pro Cys Phe Leu Pro Cys Lys Lys  
 725 730 735  
 Asp Cys Ile Val Thr Ala Phe Ser Glu Trp Thr Pro Cys Pro Arg Met  
 740 745 750  
 Cys Gln Ala Gly Asn Ala Thr Val Lys Gln Ser Arg Tyr Arg Ile Ile  
 755 760 765  
 Ile Gln Glu Ala Ala Asn Gly Gly Gln Glu Cys Pro Asp Thr Leu Tyr  
 770 775 780  
 Glu Glu Arg Glu Cys Glu Asp Val Ser Leu Cys Pro Val Tyr Arg Trp  
 785 790 795 800  
 Lys Pro Gln Lys Trp Ser Pro Cys Ile Leu Val Pro Glu Ser Val Trp  
 805 810 815

Gln Gly Ile Thr Gly Ser Ser Glu Ala Cys Gly Lys Gly Leu Gln Thr  
 820 825 830  
 Arg Ala Val Ser Cys Ile Ser Asp Asp Asn Arg Ser Ala Glu Met Met  
 835 840 845  
 Glu Cys Leu Lys Gln Thr Asn Gly Met Pro Leu Leu Val Gln Glu Cys  
 850 855 860  
 Thr Val Pro Cys Arg Glu Asp Cys Thr Phe Thr Ala Trp Ser Lys Phe  
 865 870 875 880  
 Thr Pro Cys Ser Thr Asn Cys Glu Ala Thr Lys Ser Arg Arg Arg Gln  
 885 890 895  
 Leu Thr Gly Lys Ser Arg Lys Lys Glu Lys Cys Gln Asp Ser Asp Leu  
 900 905 910  
 Tyr Pro Leu Val Glu Thr Glu Leu Cys Pro Cys Asp Glu Phe Ile Ser  
 915 920 925  
 Gln Pro Tyr Gly Asn Trp Ser Asp Cys Ile Leu Pro Glu Gly Arg Arg  
 930 935 940  
 Glu Pro His Arg Gly Leu Arg Val Gln Ala Asp Ser Lys Glu Cys Gly  
 945 950 955 960  
 Glu Gly Leu Arg Phe Arg Ala Val Ala Cys Ser Asp Lys Asn Gly Arg  
 965 970 975  
 Pro Val Asp Pro Ser Phe Cys Ser Ser Ser Gly Tyr Ile Gln Glu Lys  
 980 985 990  
 Cys Val Ile Pro Cys Pro Phe Asp Cys Lys Leu Ser Asp Trp Ser Ser  
 995 1000 1005  
 Trp Gly Ser Cys Ser Ser Ser Cys Gly Ile Gly Val Arg Ile Arg Ser  
 1010 1015 1020  
 Lys Trp Leu Lys Glu Lys Pro Tyr Asn Gly Gly Arg Pro Cys Pro Lys  
 1025 1030 1035 1040  
 Leu Asp Leu Lys Asn Gln Val His Glu Ala Val Pro Cys Tyr Ser Glu  
 1045 1050 1055  
 Cys Asn Gln Tyr Ser Trp Val Val Glu His Trp Ser Ser Cys Lys Ile  
 1060 1065 1070  
 Asn Asn Glu Leu Arg Ser Leu Arg Cys Gly Gly Gly Thr Gln Ser Arg  
 1075 1080 1085  
 Lys Ile Arg Cys Val Asn Thr Ala Asp Gly Glu Gly Gly Ala Val Asp  
 1090 1095 1100  
 Ser Asn Leu Cys Asn Gln Asp Glu Ile Pro Pro Glu Thr Gln Ser Cys  
 1105 1110 1115 1120  
 Ser Leu Met Cys Pro Asn Glu Cys Val Met Ser Glu Trp Gly Leu Trp  
 1125 1130 1135  
 Ser Lys Cys Pro Gln Ser Cys Asp Pro His Thr Met Gln Arg Arg Thr  
 1140 1145 1150  
 Arg His Leu Leu Arg Pro Ser Leu Asn Ser Arg Thr Cys Ala Glu Asp  
 1155 1160 1165  
 Ser Gln Val Gln Pro Cys Leu Leu Asn Glu Asn Cys Phe Gln Phe Gln  
 1170 1175 1180  
 Tyr Asn Leu Thr Glu Trp Ser Thr Cys Gln Leu Ser Glu Asn Ala Pro  
 1185 1190 1195 1200  
 Cys Gly Gln Gly Val Arg Thr Arg Leu Leu Ser Cys Val Cys Ser Asp  
 1205 1210 1215  
 Gly Lys Pro Val Ser Met Asp Gln Cys Glu Gln His Asn Leu Glu Lys  
 1220 1225 1230  
 Pro Gln Arg Met Ser Ile Pro Cys Leu Val Glu Cys Val Val Asn Cys  
 1235 1240 1245  
 Gln Leu Ser Gly Trp Thr Ala Trp Thr Glu Cys Ser Gln Thr Cys Gly  
 1250 1255 1260

His Gly Gly Arg Met Ser Arg Thr Arg Phe Ile Ile Met Pro Thr Gln  
 1265 1270 1275 1280  
 Gly Glu Gly Arg Pro Cys Pro Thr Glu Leu Thr Gln Glu Lys Thr Cys  
 1285 1290 1295  
 Pro Val Thr Pro Cys Tyr Ser Trp Val Leu Gly Asn Trp Ser Ala Cys  
 1300 1305 1310  
 Lys Leu Glu Gly Gly Asp Cys Gly Glu Gly Val Gln Ile Arg Ser Leu  
 1315 1320 1325  
 Ser Cys Met Val His Ser Gly Ser Ile Ser His Ala Ala Gly Arg Val  
 1330 1335 1340  
 Glu Asp Ala Leu Cys Gly Glu Met Pro Phe Gln Asp Ser Ile Leu Lys  
 1345 1350 1355 1360  
 Gln Leu Cys Ser Val Pro Cys Pro Gly Asp Cys His Leu Thr Glu Trp  
 1365 1370 1375  
 Ser Glu Trp Ser Thr Cys Glu Leu Thr Cys Ile Asp Gly Arg Ser Phe  
 1380 1385 1390  
 Glu Thr Val Gly Arg Gln Ser Arg Ser Arg Thr Phe Ile Ile Gln Ser  
 1395 1400 1405  
 Phe Glu Asn Gln Asp Ser Cys Pro Gln Gln Val Leu Glu Thr Arg Pro  
 1410 1415 1420  
 Cys Thr Gly Gly Lys Cys Tyr His Tyr Thr Trp Lys Ala Ser Leu Trp  
 1425 1430 1435 1440  
 Asn Asn Asn Glu Arg Thr Val Trp Cys Gln Arg Ser Asp Gly Val Asn  
 1445 1450 1455  
 Val Thr Gly Gly Cys Ser Pro Gln Ala Arg Pro Ala Ala Ile Arg Gln  
 1460 1465 1470  
 Cys Ile Pro Ala Cys Arg Lys Pro Phe Ser Tyr Cys Thr Gln Gly Gly  
 1475 1480 1485  
 Val Cys Gly Cys Glu Lys Gly Tyr Thr Glu Ile Met Lys Ser Asn Gly  
 1490 1495 1500  
 Phe Leu Asp Tyr Cys Met Lys Val Pro Gly Ser Glu Asp Lys Lys Ala  
 1505 1510 1515 1520  
 Asp Val Lys Asn Leu Ser Gly Lys Asn Arg Pro Val Asn Ser Lys Ile  
 1525 1530 1535  
 His Asp Ile Phe Lys Gly Trp Ser Leu Gln Pro Leu Asp Pro Asp Gly  
 1540 1545 1550  
 Arg Val Lys Ile Trp Val Tyr Gly Val Ser Gly Gly Ala Phe Leu Ile  
 1555 1560 1565  
 Met Ile Phe Leu Ile Phe Thr Ser Tyr Leu Val Cys Lys Lys Pro Lys  
 1570 1575 1580  
 Pro His Gln Ser Thr Pro Pro Gln Gln Lys Pro Leu Thr Leu Ala Tyr  
 1585 1590 1595 1600  
 Asp Gly Asp Leu Asp Met  
 1605

<210> 7  
 <211> 5080  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> 3, 7, 14, 15  
 <223> n = A,T,C or G



<400> 7

ganccanagt	agcnnccggg	ttgccagacg	ctggaatggg	tggtcttccg	acacacacca	60
ccatctttct	tgcgctcggg	aagctcgggg	ctcagcgggt	cccagagggt	acggcggcgg	120
ctctggcgag	acgggaatag	gcaagtcaag	aggctgaaaa	atctgaagca	tgtttccaaa	180
gagcaacct	acagtcactt	gctgggtatg	gaggagcatg	aggaagctct	ttctattgct	240
ttctctcttg	ctgtcccatg	cagctcattt	ggaaggcaaa	aaggataatc	agttcatctg	300
gaaaccagg	ccgtggggaa	ggtgtacagg	agactgtggg	cccggaggag	tccagagtcg	360
ggcagtggtg	tgttttcatg	ttgacgggtg	gacaagtcac	ctgtctaact	gtggtgagag	420
caacaggcct	ccaaaggaaa	gaagtgtgtt	ccgagtttgt	gactggcaca	gtgacctctt	480
tcagtgagg	gtttctgact	ggcaccactg	tgtgcttggt	ccttacgctc	gcgggtgaagt	540
caagcctcgg	actgcagagt	gtgtgacggc	tcagcatgga	ctgcagcacc	ggatgggtcg	600
ctgcattcag	aagctgaacc	gaactgtggg	tgcaaatgaa	atatgcgaac	actttgccct	660
tcagcctcct	acagaacagg	cttgccctcat	tccttgtccc	cgggattgtg	tagtatctga	720
gttctttacca	tggtccaact	gtagcaagg	atgtgggaag	aaattgcagc	atagaactcg	780
cgcggtcata	gctccccctc	tctttgggtg	tttgcaatgt	ccaaatctga	ctgagtcaag	840
agcctgtgat	gctcccattt	cctgtcctct	tggggaagag	gaatatacat	ttagccttaa	900
ggttgaggaca	tggagtaaat	gcagactgcc	tcactcttaa	gaaattaatc	caagcgggaag	960
aaactgttctg	gatttttaact	ctgattcaaa	tgagcgagtc	acctttaaac	atcaaagtta	1020
caaagcacat	catcattcga	agtcttgggc	aatagagata	ggttatcaaa	cccggcagg	1080
ttcgtgtaca	agaagtgatg	gacaaaatgc	tatgttaagc	ctttgccttc	aagattcctt	1140
cccattgact	gttcagtcct	gcacatgcgc	caaagactgt	gaaacctccc	agtgggtcctc	1200
ctggagcccc	tgctccaaga	catgccgttc	aggagctctc	ttgccaggat	ttaggagcag	1260
gagccggaac	gtgaagcaca	tggctatttg	aggtggaaag	gagtgtcctg	aacttcttga	1320
gaaagaggcc	tgcatgtgtg	aaggagaact	tctgcagcaa	tgctccagg	attcctggag	1380
aacttctgaa	tggaaagaat	gccaagtctc	tctcctcctc	gagcagcagg	atccccactg	1440
gcatgtgacg	ggaccctgtg	gtggcggtgg	gatccagacc	cgggaggtgt	actgtgcccc	1500
gagcgtacca	gcagctgccc	cactgagggc	caaggaagtc	tctagacctg	tggaaaaggc	1560
attatgtgtg	ggaccgcgcc	cgttgccctc	tcagctctgc	aatatccctt	gtcttacgga	1620
ctgcatagta	tcttcttggt	cagcctgggg	cctgtgcac	catgaaaact	gtcatgaacc	1680
tcaggggaaa	aaaggattta	gaacgaggca	gcgccatgtc	ctcatggaat	ctacagggcc	1740
tgcagggcat	tgccctcatt	tgggtggagt	tggttcttgt	gaggatccaa	tgtgctaccg	1800
atggctggca	tcagaaggga	tctgtttccc	tgatcatgga	aaatgtggcc	tgggacatcg	1860
tattctgaag	gccgtctgcc	agaatgaccg	cggagaagat	gtatcaggga	gtctttgccc	1920
agttccccct	cctcctgaga	ggaagtcttg	tgaaattccc	tgccgaatgg	actgtgtgct	1980
gagcagtggt	acggagtggg	catcctgttc	ccagtcctgt	tcaaataaaa	actcagatgg	2040
gaaacagacc	aggtcaagaa	ctatcctggc	actggctggg	gaaggtggaa	agccatgtcc	2100
ccctagtccg	gctctccaag	agcatcggtt	gtgtaatgac	cattcctgta	tgcagcttca	2160
ctgggagaca	tgccttggg	gcccttggtc	tgaggacaca	ttggtaactg	cccttaatgc	2220
aaccattggc	tggaatggag	aagccacgtg	tgggtgtagg	attcagactc	ggagagtctt	2280
ctgtgtcaag	agtcacgtgg	gacaagtaat	gacaaaaga	tgtccagatt	ctactcgacc	2340
tgaactgtg	cgcctctgtt	ttctcccatt	caaaaaagac	tgtattgtga	ctgctttcag	2400
tgagtggaca	ccctgcccac	ggatgtgcca	agcaggaaat	gccacagtaa	aacagtctcg	2460
atacagaatc	atcatccaag	aagcagccaa	tggaggccag	gaatgcccg	ataccttata	2520
tgaggagaga	gagtgtgaag	atgtttcctt	gtgtcctgta	tatcgggtga	agccacagaa	2580
atggagccct	tgcactcttag	tgccagagtc	tgtctggcag	ggaataacgg	gcagcagtga	2640
agcctgtgga	aaggggttac	aaacaagagc	tgtctcatgc	atctctgatg	acaaccgggtc	2700
agcagaaatg	atggaatgcc	tcaagcagac	aaacggcatg	cctctccttg	tgcaagaatg	2760
cacagtccca	tgctcgagaag	actgcacctt	cactgcttgg	tccaagttaa	cgcctgtctc	2820
cacgaactgt	gaagccacaa	aaagttagcg	gcgacagctc	acagggaaaa	gcagaaagaa	2880
ggagaaatgc	caggattctg	acctttaccc	tctagtggag	acagaactat	gtccttgtga	2940
tgaatttata	tcccaacctt	atggaaactg	gtcagattgc	attcttccag	aaggcagaag	3000
ggagcctcac	cgaggactgc	gggtacaagc	agacagcaaa	gaatgtggag	aaggcctgcg	3060
ctttcgagca	gtagcctgtt	ctgataaaaa	tggaaagacct	gttgacctct	ccttctgcag	3120
cagctctggt	tacattcaag	aaaaatgtgt	cattccctgc	ccatttgatt	gcaagttaag	3180
cgattggtct	agttgggggt	cttgacgttc	atcttgtgga	attggagtga	gaattcgatc	3240
caaattggcta	aaagaaaaac	cttacaatgg	aggacgacca	tgtcccaaac	tggtatctcaa	3300

